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A NEW ENDEMIC FOREST SKINK (SQUAMATA; SCINCIDAE; *Sphenomorphus*) FROM THE SANDSTONE ECOSYSTEM OF THE KHORAT PLATEAU, THAILAND

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Abstract

A new Forest Skink, belonging to the *Sphenomorphus stellatus* complex, was discovered in the unique forested sandstone ecosystem of the Khorat Plateau in northeastern Thailand. This new skink was recovered as the sister species to the other Indochinese skinks, *S. phuquocensis* + *S. annamiticus*, based on a phylogeny using 1,184 base pairs of 12S and 16S. A multiple factor analysis (MFA) based on a concatenated dataset comprised of size-corrected morphometric, meristic, and color pattern characters revealed this species' isolated position in morphospace with respect to all other species in the *S. stellatus* complex. This is the fourth endemic lizard species reported from the Khorat Plateau and adds to a growing list of endemic species across a broad range of taxa. As such, this region desperately needs legal protection and increased field-based systematic research to uncover more unrealized species on this plateau in need of description and protection.

Keywords: Indochina, integrative taxonomy, lizard, Reptilia, Sphenomorphinae, systematics

Introduction

The Khorat Plateau is a massive sandstone uplift in northeastern Thailand that purportedly has

been a region of speciation and endemism since the Early Cretaceous (Fernandez *et al.* 2009, Ridd *et al.* 2011, Meynell 2017, Yang & Grote

2018, Shen & Siritongkham 2020). Its varied climate and unique geology continue to support a wide range of endemic species across a broad taxonomic spectrum—and amphibians and reptiles are no exception (Stuart & Chuaynkern 2007, Vogel & David 2019, Köhler *et al.* 2021, Pauwels *et al.* 2021, Bernstein *et al.* 2022, Poyarkov *et al.* 2021, 2023; Wanchai *et al.* 2024). However, to date, no members of the Scincidae (skinks) are among them. Skinks of the *Sphenomorphus stellatus* complex (*sec.* Quah & Grismer 2025) comprise a monophyletic group of six generally robust species that fragmentally range from northern Borneo through the Thai-Malay Peninsula and Thailand, eastward through Cambodia to southern and central Vietnam (Fig. 1). All are generally secretive and wary, and as such, some species are known from only their holotypes (Grismer *et al.* 2019, 2020). Species of

the *S. stellatus* complex are terrestrial to scansorial and frequent a broad array of forested microhabitats ranging from basking sites on tree trunks as high as 3–5 m above the ground to outcroppings of granite rock. These wary skinks are difficult to approach and various species are known to take refuge beneath exfoliating tree bark, in earthen burrows, within rock cracks and crevices, in accumulated resin within human-made tree cavities, beneath surface debris in leaf litter (Darevsky & Ngyuen 1983, Grismer 2011, Vassilieva *et al.* 2016, Grismer *et al.* 2019, 2020), and have even been found in pit-fall traps (Stuart & Emmet 2006). Given this rather broad range of microhabitat and refugia preference, it was not too surprising to find a new population of this clade inhabiting sandstone cracks and crevices on the northeastern edge of the Khorat Plateau.

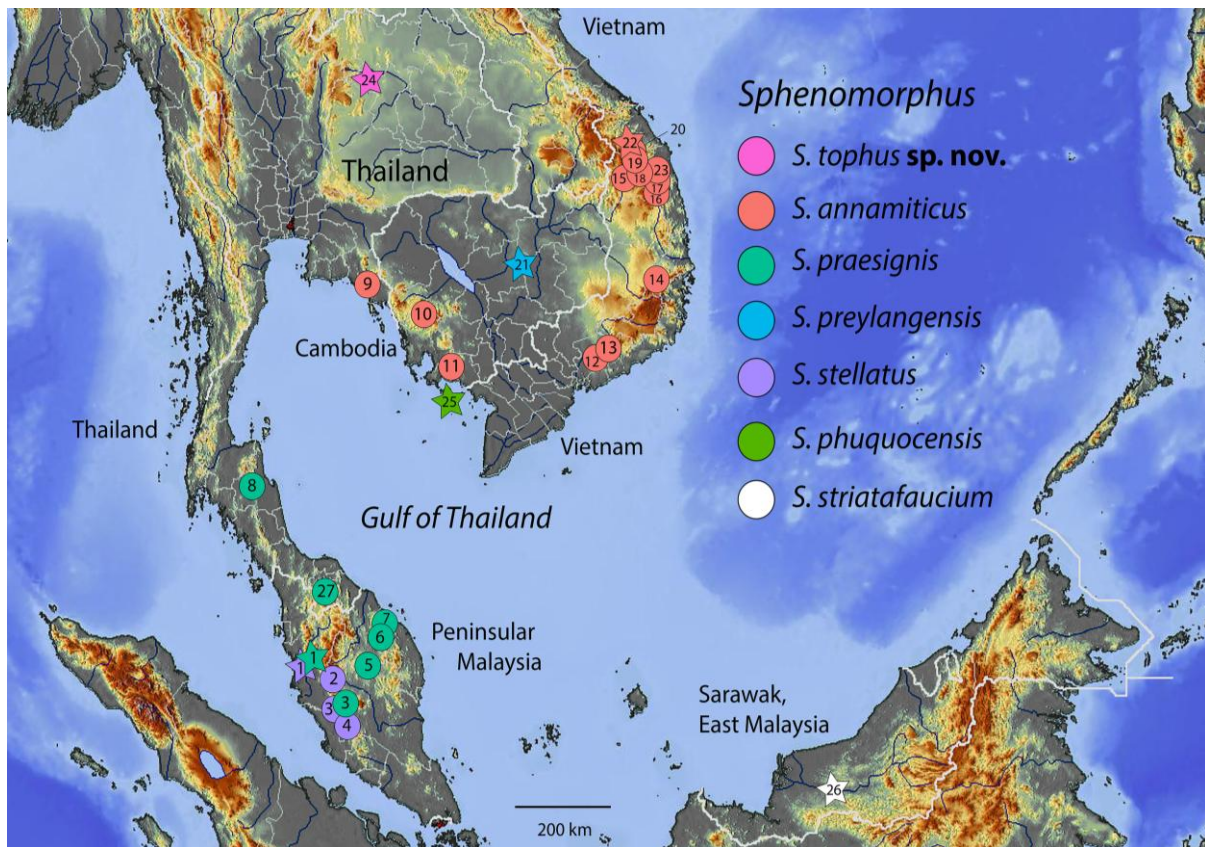


Figure 1. Known distribution and localities for *Sphenomorphus annamiticus*, *S. phuquocensis*, *S. praesignis*, *S. preylangensis*, *S. stellatus*, *S. striatafaucium*, and *S. tophus* sp. nov. Stars represent type localities. **Peninsular Malaysia:** ¹Bukit Larut, Perak; ²Cameron Highlands, Pahang; ³Fraser's Hill, Pahang; ⁴Genting Highlands, Pahang; ⁵Gn. Tahan, Pahang; ⁶Gn. Lawit, Terengganu; ⁷Gn. Tebu, Terengganu. **East Malaysia:** ²⁶Nanga Tekalit Sarawak. **Thailand:** ⁸Khao Wang Hip, Nakhon Si Thammarat Province; ⁹Khao Soi Dao Wildlife Sanctuary, Chantaburi Province; ²⁴Thanm Gwang, Khon Kaen Province. **Cambodia:** ¹⁰Chum Noab, Koh Kong Province; ¹¹Bokor National Park, Kampot Province; ²¹Phnom Chi, Prey Lang Wildlife Sanctuary, Kampong Thom Province. **Vietnam:** ¹²Ma Da, Dong Nai Province; ¹³Cat Tien, Dong Nai Province; ¹⁴Dalat, Annam, Lam Dong Province; ¹⁵Thac Nham, Kon Tum Province; ¹⁶Buon Luoi Village, Gia Lai Province; ¹⁷Tram Lap Village, Gia Lai Province; ^{18–20}Mang Canh Village and vicinity, Kon Tum Province; ²²Phuc-Son, Annam (now Phuoc Son District, Quang Nam Province); ²³K Bang, Gia Lai Province; ²⁵Phuquoc Island, Kien Giang Province.

A mitochondrial phylogeny based on the ribosomal RNA (rRNA) genes 12S rRNA and 16S rRNA recovered an individual of this new population to be deeply embedded within the *S. stellatus* complex but well-outside the clades of other species. In a multiple factor analysis (MFA) based on a wide range of morphological and color pattern characters, this single specimen plotted notably outside the clusters of the other species as well. Based on its phylogenetic and morphospacial relationships, its unique sandstone microhabitat preference, and the fact that it is ca. 460 km due north of the closest member of the *S. stellatus* complex—*S. annamiticus* from the Khao Soi Dao Wildlife Sanctuary, Chantaburi Province in southern Thailand—it is described below as a new species.

Materials and methods

Molecular data. We extracted total genomic DNA from ethanol-preserved muscle tissue using standard phenol-chloroform extraction procedures (Sambrook *et al.* 1989), followed by isopropanol precipitation. The 12S and 16S rRNA mitochondrial genes were amplified using a double-stranded Polymerase Chain Reaction (PCR) under the following conditions: 1.0 µl genomic DNA (10–30 µg), 1.0 µl light strand primer (10 µM), 1.0 µl heavy strand primer (10 µM), 1.0 µl dinucleotide pairs (1.5 µM), 2.0 µl 5x buffer (1.5 µM), MgCl 10x buffer (1.5 µM), 0.1 µl Taq polymerase (5u/µl), and 6.4 µl ultra-pure H₂O. PCR reactions were executed on a Bio-Rad gradient thermocycler under the following conditions: initial denaturation at 95°C for 2 min, followed by a second denaturation at 95°C for 35 s, annealing at 54–56°C for 35 s, followed by a cycle extension at 72°C for 35 s, for 31 cycles. All PCR products were visualized on a 1.0% agarose gel electrophoresis. Successful PCR products were sent to Eurogene® (Moscow) for PCR purification, cycle sequencing, sequencing purification, and sequencing using the same primers as in the amplification step (Sup. Table 1). Sequences were analyzed from both the 3' and the 5' ends separately to confirm congruence between reads. Following sequence editing, we aligned the regions with those of Grismer *et al.* (2020) using the MAFFT v7.017 (Kato & Kuma 2002) plugin under the default settings in Geneious™ (Kearse *et al.* 2012). All new sequences were uploaded to GenBank (Sup. Table 2).

Molecular analyses. Along with the new specimen from the Khorat Plateau, ingroup

sequences included seven samples of *Sphenomorphus annamiticus* from across its range in Indochina, one sample of *S. phuquocensis* from Phu Quoc Island (Vietnam), one sample of *S. stellatus* from the type locality in Peninsular Malaysia, three samples of *S. preylangensis* from the type locality in Cambodia, and 13 samples of *S. praesignis* across its range in Peninsular Malaysia. Following Linkem (2013), seven species of Indochinese *Tropidophorus* were used to root the tree (see Grismer *et al.* 2019). A Maximum Likelihood (ML) analysis was implemented in IQ-TREE (Nguyen *et al.* 2015), employing the GTR+I+G model of evolution. Ten thousand bootstrap pseudoreplicates via the ultrafast bootstrap (UFB) approximation algorithm (Hoang *et al.* 2018; Minh *et al.* 2013) were employed, and nodes having UFB values of 95 and above were considered strongly supported (Minh *et al.* 2013). A Bayesian inference (BI) analysis was carried out in MrBayes 3.2.3. (Ronquist *et al.* 2012) on XSEDE using the CIPRES Science Gateway (Cyberinfrastructure for Phylogenetic Research; Miller *et al.* 2010) employing the GTR+G model of evolution using default priors. Two independent Markov chain Monte Carlo (MCMC) simulations were performed, each with four chains, three hot and one cold. We ran the MCMC simulation for 30 million generations, sampled every 3,000 generations, and discarded the first 10% of each run as burn-in. Convergence and stationarity of all parameters from both runs were checked in Tracer v1.6 (Rambaut & Drummond 2013) to ensure effective sample sizes (ESS) were above 200. Post-burn-in sampled trees from both runs were combined using the sumt function, and a 50% majority rule consensus tree was constructed. Nodes with Bayesian posterior probabilities (BPP) of 0.95 and above were considered highly supported (Huelsenbeck *et al.* 2001; Wilcox *et al.* 2002). Retaining ingroup taxa only, uncorrected pairwise sequence divergences were calculated in MEGA X (Tamura *et al.* 2021) using the pairwise deletion option.

Morphological data. All measurements were made with Mitutoyo™ digital calipers to the nearest 0.1 mm. Scale counts were made on the right side of the body, when possible, under a Nikon SMZ 1500 dissecting microscope. Scale terminology (Fig. 2) follows Grismer *et al.* (2019; Fig. 2). Measurements taken were snout–vent length (SVL) measured from the tip of the

rostral scale to the vent; tail length (**TAL**) measured from the vent to the tip of the tail; head length (**HL**) measured from the retroarticular process to the tip of the snout; head width (**HW**) measured at the widest point of the head posterior to the eyes; head height (**HH**) measured across the highest part of the head posterior to the eyes; snout length (**SFL**) measured from the anterior border of the orbit (not the eyeball) to the tip of the snout; distance from tip of snout to anterior border of ear opening (**STL**); eyeball diameter (**ED**) measured from the posterior to the anterior margins of the eyeball; eye to tympanum (**ET**) measured from the anterior margin of the ear opening to the posterior margin of the orbit; tympanum diameter (**TD**) measured as the vertical length across the ear opening; axilla-groin length (**AG**) measured from the anterior margin of the hind limb at its insertion point of the body to the posterior margin of the forelimb at its insertion point on the body with the upper limb sections held at right angles to the body; forelimb length (**FIL**) measured from the insertion point of the forelimb on the body to the base of the fourth finger with the brachium held at a right angle to the body; and hind limb length (**HIL**) measured from the insertion point of the hind limb on the body to the base of the fourth toe with the thigh held at a right angle to the body.

Scale counts taken were the number of supraoculars contacted by the frontoparietal (**SO**), midbody scale rows (**MB**) counted as the number of longitudinal scale rows encircling the body at a point midway between the limb insertions, paravertebral scale rows (**PV**) counted as the number of scales in a line from the nuchal scales to a point on the dorsum opposite the vent, ventral scale rows (**VS**) counted as a row of scales between the postmental and the precloacal scales, nuchal scales (**NU**) counted as the number of the scales between opposing upper secondary temporals (**ST**) on each side of the head that contact the parietals, post-parietal scales (**PPS**) counted as the number of scales contacting the parietals (**NU** plus **ST**), number of primary, secondary, and tertiary temporals (**PT**, **ST**, and **TT**, respectively), superciliaries (**SC**), supraoculars (**So**), loreals (**AL** and **PL**), preoculars (**Pr**), postsuboculars (**#**), supralabials (**SL**), infralabials (**IL**), fourth toe and finger subdigital lamellae (**TL4** and **FL4**, respectively), and number of caudal scales around the tail at the position of the tenth subcaudal scales, size of subcaudal scales, and presence or absence of

postnasal groove. Color pattern characters included the presence or absence of dark vertebral and lateral stripes, blotching on the head, labial patterning, the presence or absence of large, dark anterolateral spots, the presence or absence of dark labial sutures, and dark dorsal and subcaudal banding (bars).

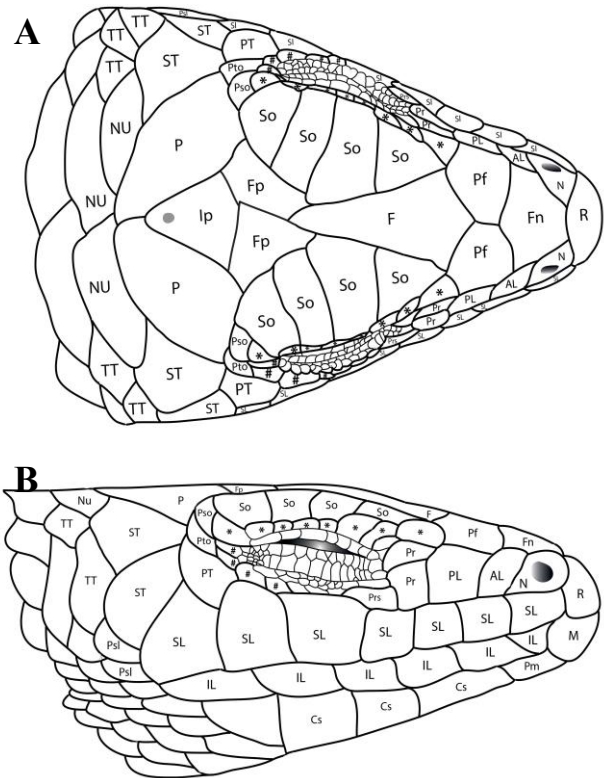


Figure 2. Head scale nomenclature and their positional relationship and size illustrated by the adult female *Sphenomorphus stellatus* LSUHC 13483 (SVL = 88.0 mm) from the type locality of Bukit Larut, Perak, Malaysia, after Grismer *et al.* (2019): (A) dorsal and (B) right lateral view. Terminology is adapted from Taylor (1935). AL = anterior loreal, Cs = chinshield; F = frontal, Fn = frontonasal, Fp = frontoparietal, IL = infralabial, Ip = interparietal, M = mental, N = nasal, Nu = nuchal, P = parietal, Pf = prefrontal, PL = posterior loreal, Pm = postmental, Pr = preocular, Prs = presubocular, PT = primary temporal, Psl = postsupralabial, Pso = postsupraocular, Pto = postocular, R = rostral, SL = supralabial, So = supraocular, ST = secondary temporal, and TT = tertiary temporal. * = superciliary and # = postsubocular. Illustration by LLG.

Color pattern data included dark vertebral and lateral stripes present or absent, dark markings on top of the head present or absent, dark transverse subcaudal bars present or absent, thin dark dorsal caudal bands present or absent, labial sutures edged in black or not, large dark anterolateral spots on the trunk present or absent,

and dark chevron gular stripes present or absent. Museum acronyms follow Sabaj (2016) except for LSUHC, La Sierra University Herpetological Collection, Riverside, California, USA, and LSUDPC, La Sierra University Digital Photo Collection, Riverside, California, USA.

Statistical analysis. All statistical analyses were conducted using R Core Team (2020). A multiple factor analysis (MFA) using the R package *FactorMineR* (Husson *et al.* 2017) and visualized using the *Factoextra* package (Kassambara & Mundt 2017) was used to compare differences and similarities in morphospace of individuals from the *Sphenomorphus stellatus* complex. The MFA used a concatenated data set comprised of nine meristic (PPS, SL, IL, SC, MB, PV, VS, TL4, and FL4), 13 size-corrected morphometric (SVL, AG, SNL, SFL, HL, HW, HH, STL, ED, ET, TD,

FIL, and HIL) and eight categorical presence-absence characters (postnasal groove, and dark vertebral and lateral stripes, dark markings on top of head, dark transverse subcaudal bars, thin dark dorsal caudal bands, dark labial sutures, large dark anterolateral trunk spots, and dark chevron gular stripes) characters for a nearly total evidence morphological dataset (Sup. Table 2). To remove potential effects of allometry in the morphometric characters, the size-correction algorithm of Chan & Grismer (2022) was used. MFA is a global, unsupervised, multivariate analysis that incorporates qualitative and quantitative data simultaneously, making it possible to include different data types in a nearly total morphological evidence environment, and all data types are standardized, preventing one data type from overleveraging the output (Grismer 2025).

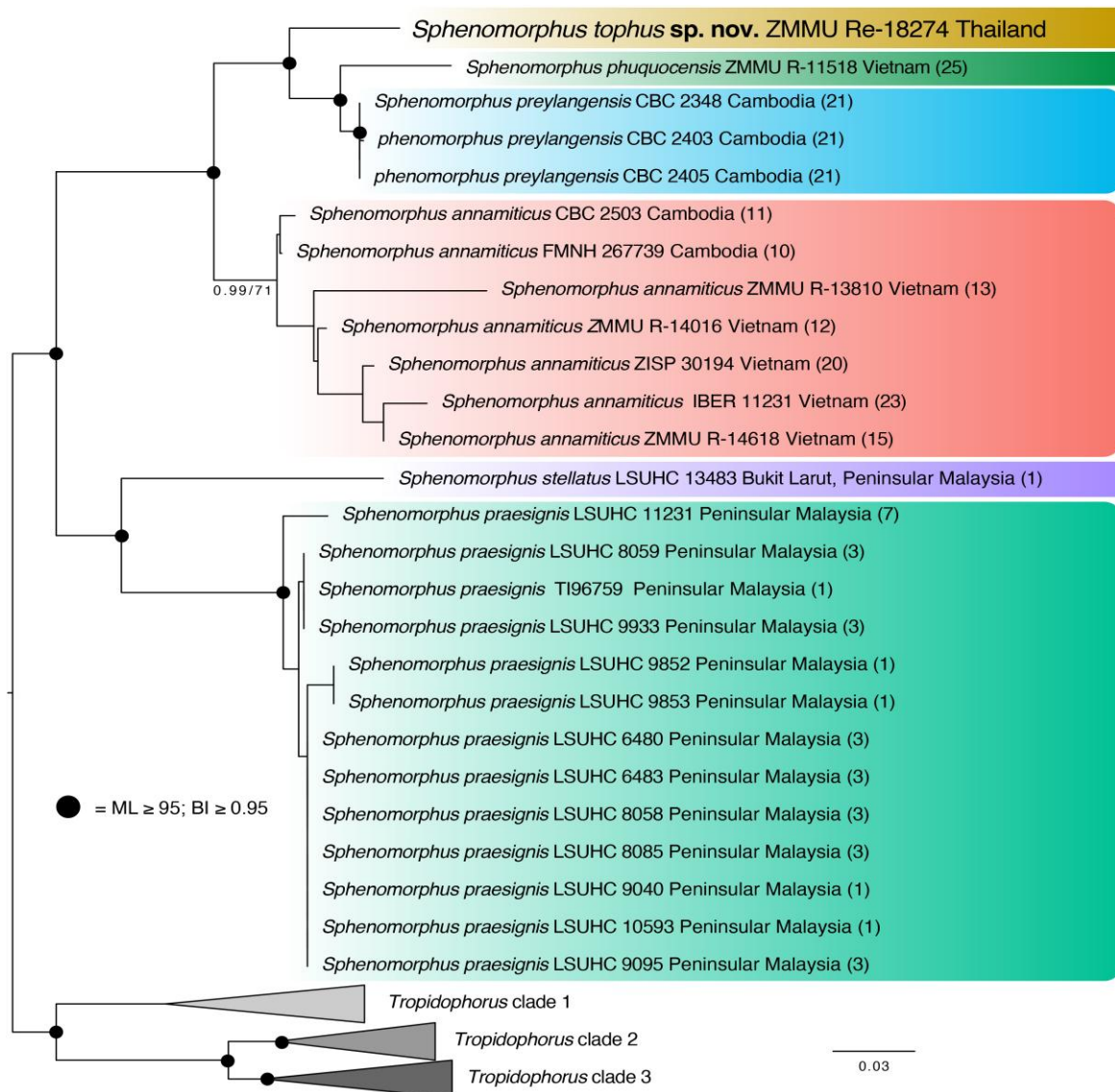


Figure 3. Maximum likelihood consensus tree. Numbers in parentheses correspond to the localities in Figure 1

Results

The ML and BI analyses recovered strongly supported trees with identical topologies (Fig. 3). The Khorat Plateau specimen was recovered as the sister species to *Sphenomorphus phuquocensis* + *S. preylangensis*. *Sphenomorphus annamiticus* is the sister species of the clade containing the former three species, which collectively are most closely related to the *S. stellatus* + *S. praesignis* clade. The Khorat Plateau specimen differs from all other species in the *S. stellatus* complex by an uncorrected pairwise sequence divergence of 3.9% to 14.0 (*S. annamiticus* – *S. phuquocensis*; Table 1). In the MFA, the Khorat Plateau specimen was compared to its closest relatives *S. annamiticus*, *S. phuquocensis*, and *S. preylangensis* (Fig. 3). The Khorat Plateau specimen was not embedded within the plots of any other *Sphenomorphus* species along the ordination of the first two dimensions (Fig. 4A). It was separated from *S. stellatus*, *S. annamiticus*, *S. phuquocensis*, *S. striatafaucium*, and *S. praesignis* along dimension 1 and from *S. stellatus*, *S. preylangensis*, and *S. praesignis* along dimension 2. Dimension 1 recovered 28.3% of the variation

in the dataset, and dimension 2 recovered an additional 17.2%. The meristic and morphometric data contributed nearly equally to the variation in the dataset in dimension 1, followed by the color pattern data, which recovered most of the variation in dimensions 2–5. The contribution of all the data types to the variation in dimensions 1–5 is presented in Figure 4B. A sample size of one does not permit a non-parametric permutation of analysis of variance (PERMANOVA) to allow a statistical evaluation of the Khorat Plateau specimen's morphospacial position with respect to the other species.

Table 1. Uncorrected pairwise sequence divergence% among species of the *Sphenomorphus stellatus* complex based on 1184 bp of 12S and 16S rRNA.

Species	1	2	3	4	5
1 <i>S. praesignis</i>					
2 <i>S. preylangensis</i>	10.7				
3 <i>S. phuquocensis</i>	12.8	3.4			
4 <i>S. annamiticus</i>	10.8	4.2	5.9		
5 <i>S. tophus</i> sp. nov.	11.6	4.1	5.5	3.9	
6 <i>S. stellatus</i>	10.6	10.7	14.0	9.8	10.6

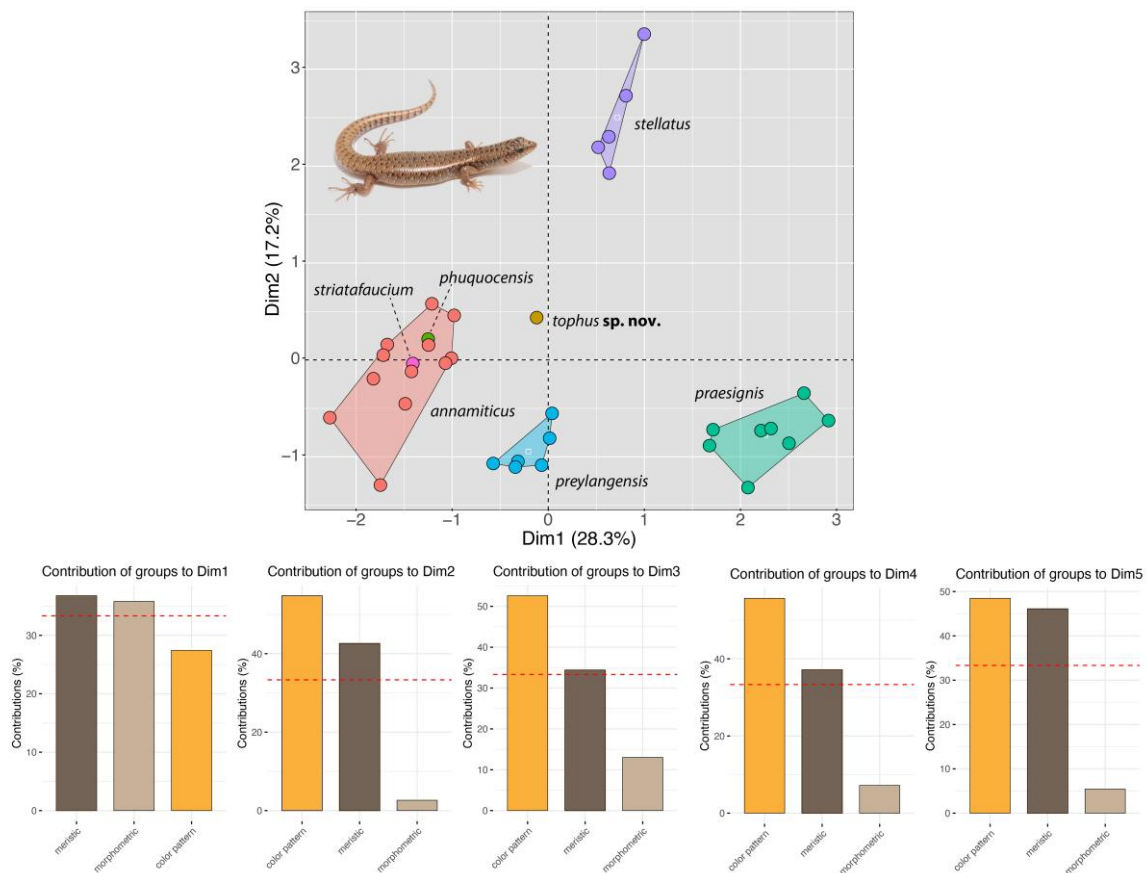


Figure 4. (Above) MFA of the species of the *Sphenomorphus stellatus* complex. (Below) Percent contribution of each data type to the first five dimensions of the MFA.

Taxonomy

Sphenomorphus tophus sp. nov.

[urn:lsid:zoobank.org:act:3A845156-87AA-47EC-9CF6-52978D8609A5]

(Figs. 2, 5, 6, 8; Sup. Tables 3, 4)

Sphenomorphus stellatus (partim)—Cox *et al.* (1998: 117) [listed for “northeastern Thailand”, see p. 117]; Chan-ard *et al.* (2015:127) [listed for “Phu Wiang, Khon Kaen Province in northeastern Thailand”].

Sphenomorphus sp.—Grismer *et al.* (2019: 398) [listed for “Phu Wiang, Khon Kaen Province in northeastern Thailand”, see Fig. 1, locality 24 in Grismer *et al.* 2019].

Holotype. Adult female ZMMU Re-18274 (field label NAP-17135), collected from Tham Gwang (16°38'15"N, 102°16'39"E), elevation 240 m asl., Khon Kaen District, Khon Kaen Province, Thailand, on 27 July 2024 by M. Naiduangchan and P. Pawangkhanant.

Diagnosis. At this juncture, *Sphenomorphus tophus* sp. nov. is separated from all other species of the *S. stellatus* complex by having the unique combination of a maximum adult SVL of 75.4 mm; head, body, and supracaudal scales smooth; frontal scale not divided; prefrontals not in contact; parietals in contact posterior to interparietal; parietals not divided; six scales bordering the parietals; four nuchals; four supraoculars; two loreals; anterior loreal not divided; loreals in contact with supralabials; no postnasal groove; eight superciliaries; superciliary row not interrupted by fourth supraocular; lower eyelid scales large; seven supralabials; seven infralabials; three pairs of chinshields; one primary temporal scale; two secondary temporals; upper secondary temporal large; no subtemporals; 25 midbody scale rows; 63 paravertebrals; paravertebrals slightly wider than other dorsals; 68 ventrals; two enlarged precloacals; 13 scales around tail at level of tenth subcaudal; anterior subcaudals not divided; subcaudals enlarged; 20 subdigital lamellae on fourth toe; 15 subdigital lamellae on fourth finger; no wide, dark, vertebral or lateral stripes or blotches; dark markings on top of head confined to scale edges; thin dark transverse subcaudal bars on original tail; no thin, dark, dorsal caudal bands; and labial margins faintly edged in black. Note that these characters are based on a single specimen. The acquisition of additional material may render some of these characters not truly diagnostic, and other

characters not listed here may be diagnostic (Sup. Table 4).

Description of holotype. Adult female, SVL 75.4 mm; original tail 89.4 mm; head moderate, snout slightly pointed, rounded in dorsal and lateral profile, subtriangular, slightly distinct from neck; head scales large, smooth; HL 13.3 mm longer than wide, HW 10.7 mm; head somewhat depressed, HH 5.8 mm; rostral wider than high, in contact with first supralabials, and nasals laterally, frontonasal dorsally; frontonasal as wide as long, single, in contact with nasals and first loreals laterally, prefrontals and frontal posteriorly; prefrontals separated contacting loreals laterally and first superciliaries posteriorly; frontal posteriorly elongate, subtriangular, in point contact with first superciliary, contacting first and second supraoculars and frontoparietals posteriorly; four supraoculars, first triangular, second and third rectangular, fourth hemispherical; frontoparietals divided sagittally, each in lateral contact with second, third, and fourth supraoculars laterally, and parietals and interparietal posteriorly; interparietal somewhat triangular, eyespot present posteriorly; parietals in medial contact posterior to interparietal, contacting upper second supratemporal laterally and nuchals posteriorly; six scales bordering posterolateral margins of parietals; four nuchals in contact with parietals; 7 (R,L) supralabials, sixth and seventh largest and equal in size, fifth below center of eye; nostril in lower part of nasals; nasals large, in broad contact with first supralabials and point contact with second supralabials ventrally, first loreal posteriorly; two undivided loreals, first square and second more rectangular, contacting supralabials ventrally; second loreal in contact with second and third supralabials, preoculars posteriorly, first superciliary and frontonasal dorsally; two preoculars, lower much larger than upper; eight (R,L) superciliaries not interrupted by fourth supraocular; two presuboculars; lower eyelid bearing large scales; one postsupraocular in ventral contact with postsubocular and posterior contact with parietal; postsubocular contacting primary temporal posteroventrally, upper secondary temporal posteriorly, and parietal medially; three postsuboculars, first two contacting fifth and sixth supralabials; one postsupraocular; one primary temporal, two secondary temporals; two tertiary temporals; two postsupralabials; seven (R,L) infralabials, first smallest; mental large, hemispherical; postmental large, single; three pairs of large chinshields in

broad contact with supralabials; second pair in point contact medially, third pair separated by three gulars; external ear opening large, vertically elongate, vertical diameter 2.1 mm, lacking anterior lobules; tympanum deeply recessed.

Body scales smooth, cycloid, imbricate; dorsals larger than ventrals and flank scales; paravertebrals slightly larger than adjacent dorsals; 25 longitudinal scale rows around midbody; 63 slightly enlarged paravertebral scale rows not interrupted by smaller scales; 68 ventrals; two enlarged, medial, precloacals; subcaudals similar in size to dorsal caudals, larger than lateral caudals; limbs robust in stature, in contact when adpressed; palmar and plantar scales low, rounded, smooth; single row of supradigitals; 15 (R, L) smooth, subdigital lamellae on fourth finger; 20 (L, R) smooth, subdigital lamellae on fourth toe.

Coloration in life. Fig. 5. Dorsum, head, flanks, limbs and tail light-brown overlain with variously separated darker scales bearing a yellowish posterior countershading producing stellate appearance; light-colored countershading on flanks is white; head plates are thickly edged in black; scattered dark-colored markings on dorsal surfaces of limbs; thin, wavy, broken dark-colored bands on dorsal surface of tail; venter generally immaculate tan-yellow; broken dark-colored subcaudal crossbars.

Etymology. The specific epithet ‘*tophus*’ is a Latin noun given in apposition, meaning “sandstone,” “porous rock”. The name is given in reference to the natural history of the new species, in that it is the only member of the *S. stellatus* group known to date that is strictly associated with sandstone habitats.

Suggested common names: Khorat Plateau Forest Skink (in English), จิ้งเหลนภูเขาหินทราย (Jing lhen phu khao hin sai, in Thai), and Короткий древесный сцинк (Koratskiy drevesnyi stsink, in Russian).

Comparison. Given that *Sphenomorphus phuquocensis*, *S. striatafaucium*, and *S. tophus* sp. nov. are only known from single specimens, univariate statistical analyses are not possible, although the available meristic data for all species are presented in the Sup. Table 3 and its summary statistics in the Sup. Table 4. Therefore, the following comparisons are based on the less intraspecifically variable color pattern characters.

Sphenomorphus tophus sp. nov. is most closely related to sister species *Sphenomorphus*

phuquocensis and *S. preylangensis* but differs from the former in lacking a postnasal groove and from the latter in lacking thin, dark-colored dorsal caudal bands. From *S. striatafaucium*, it differs by having, as opposed to lacking, large dark-colored blotches on the top of the head, having, as opposed to lacking, dark-colored transverse subcaudal bars, and lacking dark-colored chevron-shaped stripes on the throat.

Sphenomorphus tophus sp. nov. differs from *S. annamiticus* in lacking, as opposed to having, wide, dark-colored lateral and vertebral stripes, and thin dark-colored dorsal caudal bands. It differs from *S. stellatus* in having large dark-colored blotches instead of small speckles on the top of the head, having as opposed to lacking, dark-colored transverse subcaudal bars, and labial sutures edged in black. From *S. praesignis*, it differs in lacking as opposed to having thin dark-colored dorsal caudal bands and large dark-colored anterolateral trunk spots.

Distribution. *Sphenomorphus tophus* sp. nov. is currently known only from the type locality of Phu Wiang Mountain, Tham Gwang, Khon Kaen Province, Thailand (Fig. 1).

Natural history. *Sphenomorphus tophus* sp. nov. specimens were observed—but not collected—from 200–670 m asl in deciduous to dry evergreen forests among outcroppings of sandstone rock (Fig. 7). The holotype was found during the evening, anchored deep inside in a narrow sandstone crevice among an outcropping near a small rocky stream, and regurgitated a large Huntsman spider (*Heteropoda* sp.) after being collected. *Sphenomorphus tophus* sp. nov. is an active diurnal species seen on the ground, tree trunks, and sandstone rocks (Fig. 8). Observations suggest this species has a general habitat preference, as we observed skinks on sandstone rocks near streams, in crevices on cliffs, beneath boulders, and on the trunks of large trees. All were observed to be motionless but quickly retreated out of sight upon our approach. Skinks were abundant during July through October of 2023 and 2024, but not observed during January of 2025. An uncollected specimen was observed basking near a large sandstone crevice in the morning at approximately 1030 and again at approximately 1620 during the late afternoon. *Trimeresurus* cf. *macrops* Kramer, 1977; *Calotes emma* Gray, 1845, and *Tropidophorus* cf. *matsuii* Hikida, Orlov, Nabhitabhata & Ota, 2002 were also observed at the type locality.

Plate 1

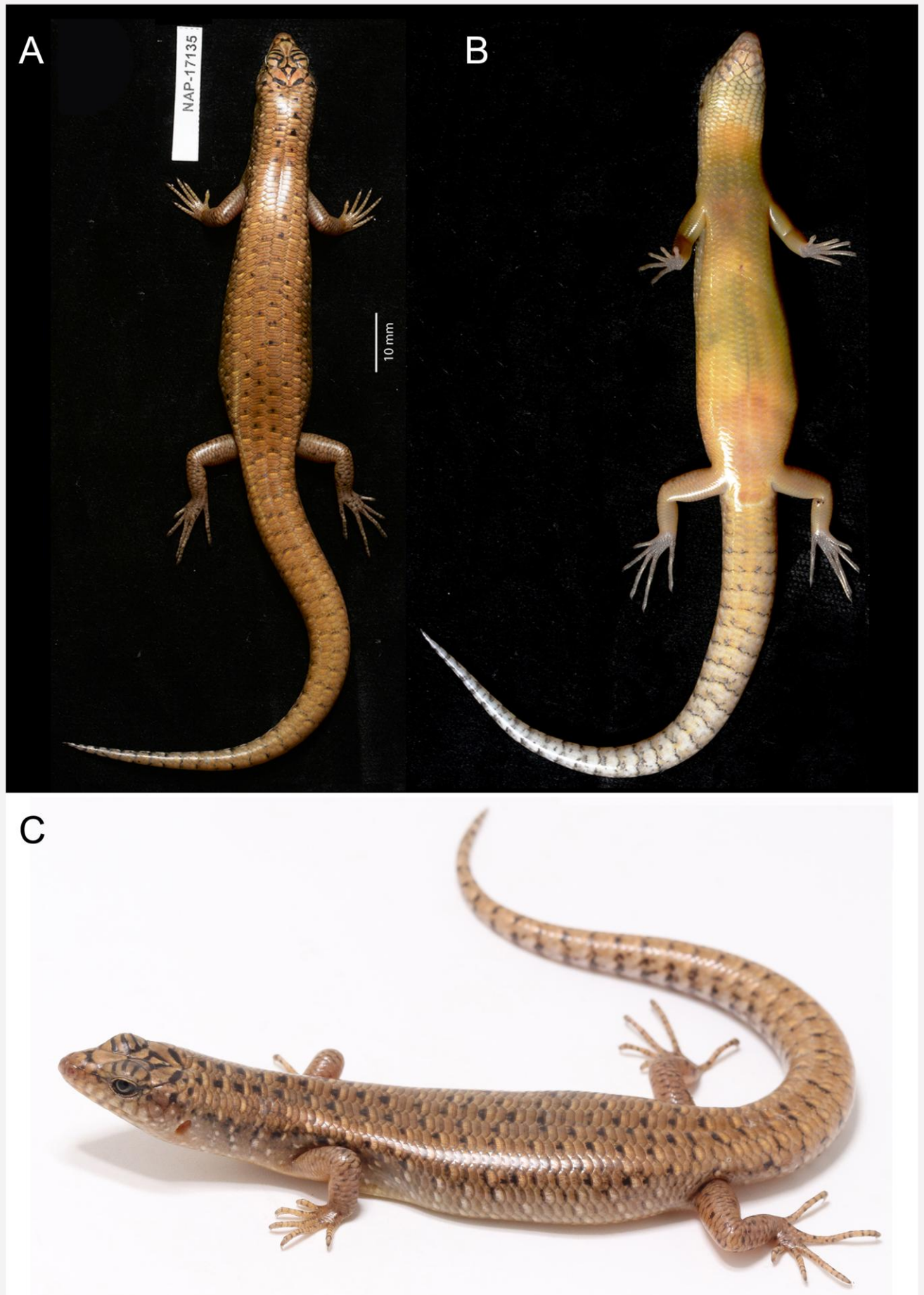


Figure 5. *Sphenomorphus tophus* sp. nov. holotype (ZMMU Re-18274): (A) dorsal and (B) ventral views of the full body (© Photo: N. Poyarkov); (C) Left dorsolateral view in life (© Photo: P. Pawangkhanant)

Plate 2

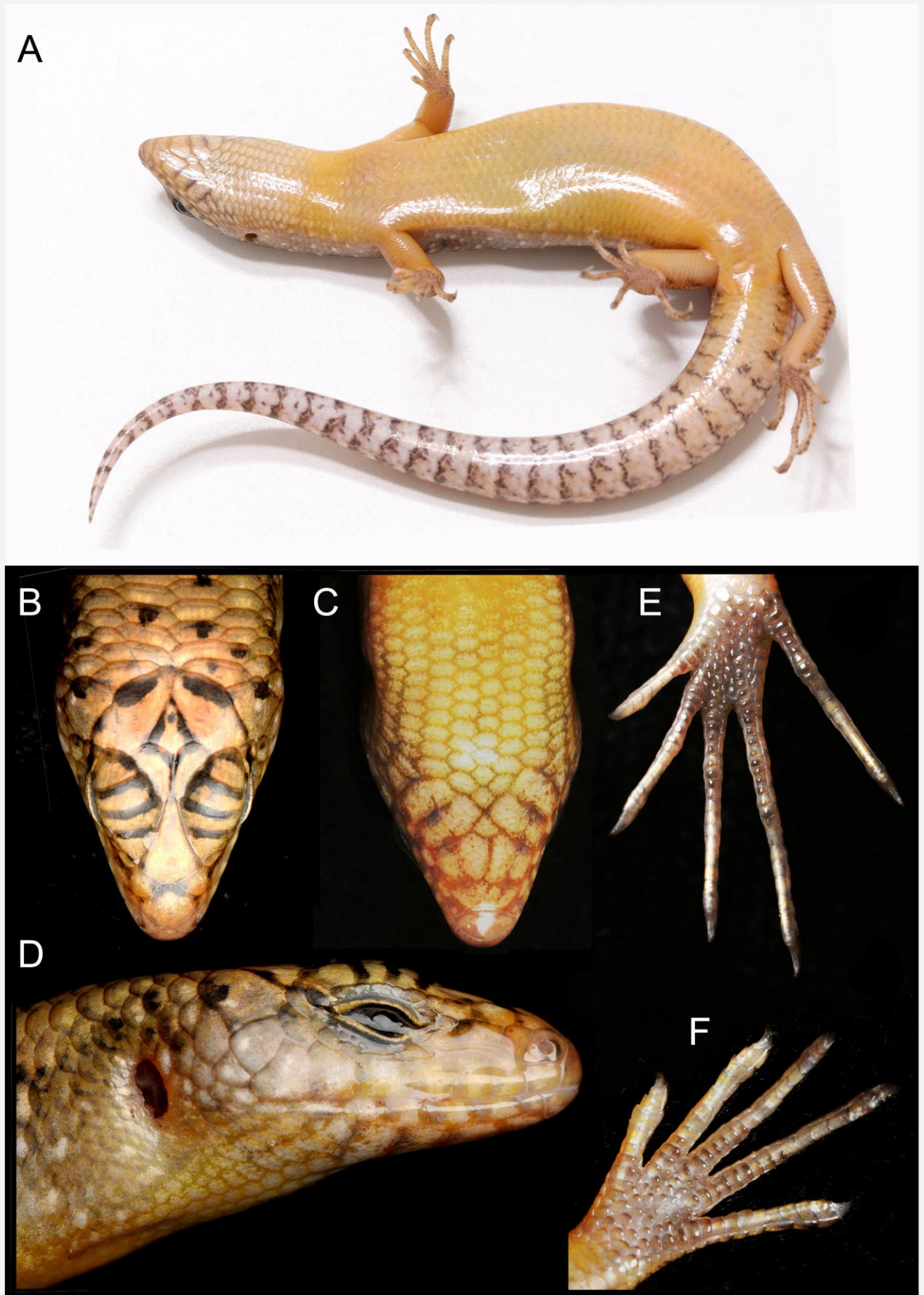


Figure 6. *Sphenomorphus tophus* sp. nov. holotype (ZMMU Re-18274): (A) ventral view of the full body in life; (B) dorsal, (C) ventral, and (D) lateral (right) view of the head; (E) ventral view of the right foot; (F) ventral view of the left hand; © Photo: N. Poyarkov

Plate 3



Figure 7. Forested habitat and sandstone microhabitat of *Sphenomorphus tophus* sp. nov. at the type locality in Tham Gwang, Khon Kaen District, Khon Kaen Province, Thailand.

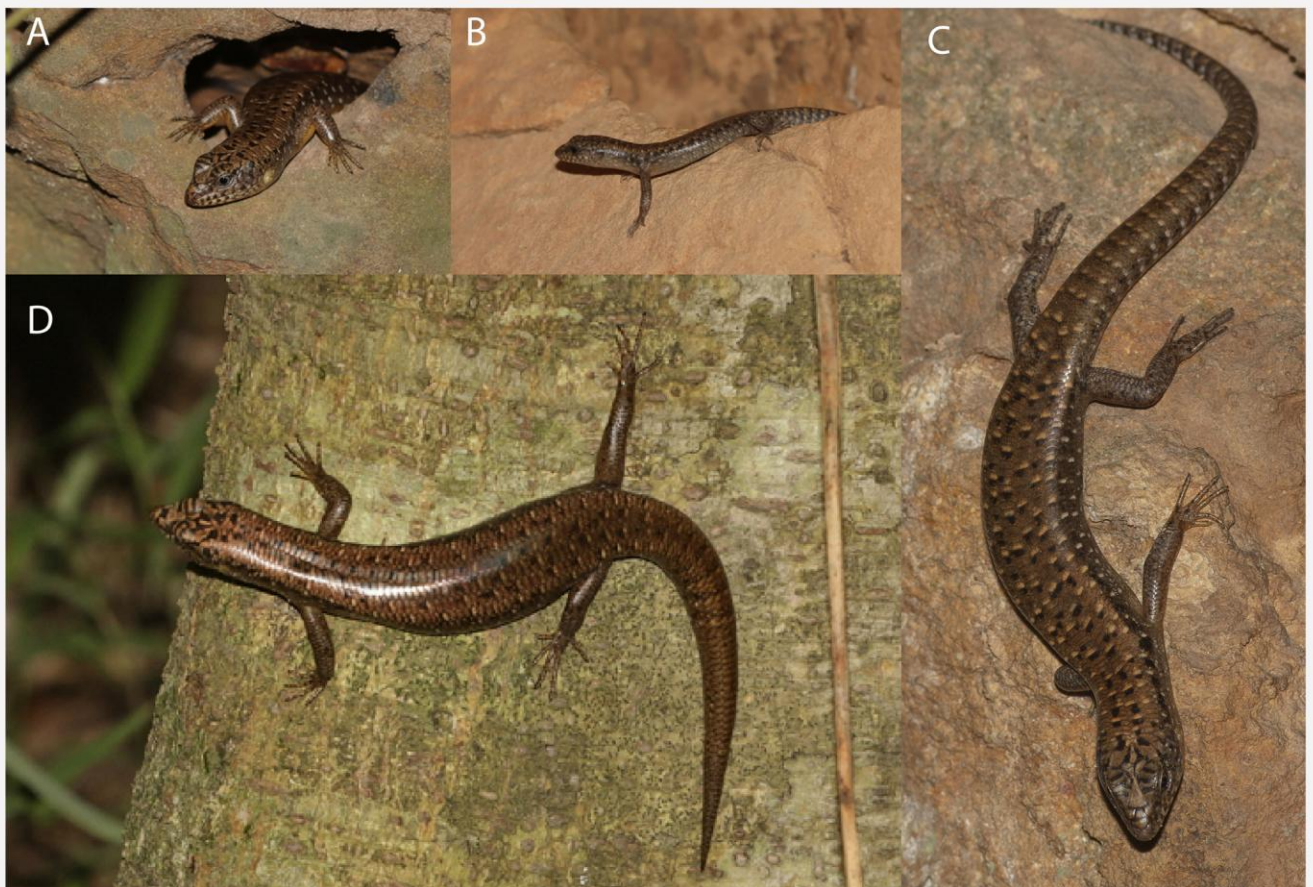


Figure 8. Uncatalogued specimens of *Sphenomorphus tophus* sp. nov. in their microhabitats in Tham Gwang, Khon Kaen District, Khon Kaen Province, Thailand: (A) an adult emerging from a hole in the sandstone; (B) a juvenile on a sandstone ridge (© Photo: I. Dugdale); (C) an adult crawling down the vertical sandstone surface (© Photo: A. Pierce); (D) an adult on the side of a tree (© Photo I. Dugdale)

Discussion

The discovery of *Sphenomorphus tophus* sp. nov. brings the total number of endemic lizards on the Khorat Plateau to four, which includes *Dixonius mekongensis* Pauwels, Panitvong, Kunya & Sumontha, 2021, *Dixonius hinchangsi* Pauwels, Das, Kunya *et al.*, 2025, and *Leiolepis glaurang* Wanchai, Rujirawan, Murdoch *et al.*, 2024. Another species of *Dixonius* Bauer, Good, & Branch, 1997 is currently being described (Rujirawan *et al.* in prep.). This indicates other endemic species may occur in this unique habitat. The selection pressures of living in a sandstone microhabitat have notably altered the behavior, morphology, and color pattern of the more arenicolous ancestor of *L. glaurang* to meet the new challenges of a sandstone microhabitat (Wanchai *et al.* 2024). The same is true for a sandstone-adapted New World xantusiid lizard *Xantusia gracilis* Grismer & Galav, 1986 (Grismer 2021). This underscores the overall effect that such a substrate may have on species that occur nowhere else. Given that *S. tophus* sp. nov. is known from only one individual, no convergent comparisons can reliably be made. Since some individuals were observed on tree trunks (Fig. 8) and the ground, it is likely that the behavior of inhabiting tree cavities and rock cracks and crevices may have served as a preadaptation for inhabiting sandstone. The long history of endemism in the Khorat Plateau (see Wanchai *et al.* 2024) should be an indication that this unique region still requires further investigation and should be afforded some degree of conservation management and other scansorial species on the plateau, such as *Gekko petricolus* Taylor, 1962, should be closely studied. The actual extent of *Sphenomorphus tophus* sp. nov.'s distribution remains unknown, although the available evidence suggests that this species is likely a narrow-range endemic of the sandstone massifs in Khon Kaen Province of Thailand. At present, the new species should be considered as "Data Deficient (DD)" following the IUCN Red List categories (IUCN Standards and Petitions Committee 2019). Further studies are required to clarify the conservation status, natural history, and distribution of *Sphenomorphus tophus* sp. nov.

Author contributions

L.L. Grismer: data analyses, figure construction, writing; M. Naiduangchan and P. Pawangkhanant: holotype collection; N. Poyarkov: gene sequencing; A. Pierce and I.

Dugdale: photographing specimens in the wild; A. Pierce, I. Dugdale, and P. Pawangkhanant: natural history observations. All authors reviewed and edited the first draft.

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Research permits

Specimen collection and animal use protocols were approved by the Institutional Ethical Committee of Animal Experimentation of the University of Phayao, Phayao, Thailand (certificate number UP-AE64-02-04-005, issued to C. Suwannapoom) and were strictly compliant with the ethical conditions of the Thailand Animal Welfare Act. Field work, including the collection of animals in the field, was authorized by the Institute of Animals for Scientific Purpose Development (IAD), Bangkok, Thailand (permit numbers U1-01205-2558 and UP-AE59-01-04-0022, issued to C. Suwannapoom).

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Supplemental data

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